

OIKE

RAW SEQUENCE LISTING

DATE: 01/03/2002

PATENT APPLICATION: US/10/016,985

TIME: 14:53:27

Input Set : A:\LEX-0273-USA SEQLIST.txt

Output Set: N:\CRF3\01032002\J016985.raw

ENTERED

4 <110> APPLICANT: Walke, D. Wade
 5 Maricar, Miranda
 6 Yu, Xuanchuan (Sean)
 7 Friddle, Carl Johan
 10 <120> TITLE OF INVENTION: Novel Human Kinase and Polynucleotides
 11 Encoding the Same
 13 <130> FILE REFERENCE: LEX-0273-USA
 15 <140> CURRENT APPLICATION NUMBER: US/10/016,985
 15 <141> CURRENT FILING DATE: 2001-12-07
 15 <150> PRIOR APPLICATION NUMBER: US 60/251,941
 16 <151> PRIOR FILING DATE: 2000-12-07
 18 <160> NUMBER OF SEQ ID NOS: 3
 20 <170> SOFTWARE: FastSEQ for Windows Version 4.0
 22 <210> SEQ ID NO: 1
 23 <211> LENGTH: 1275
 24 <212> TYPE: DNA
 25 <213> ORGANISM: Homo sapiens
 27 <400> SEQUENCE: 1
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 29 actgcccctg ggcctggtgc cgggtgtgcc cttctcactg aagacatgca ggcctgact 120
 30 ctccgcacac tggccgccag cgacgtcacc aagcactacg aactagtccg ggagctgggc 180
 31 aaaggcacct atgggaaggt tgacctggtg gtctacaagg gcacaggcac aaaaatggca 240
 32 ctgaagtttg tgaacaagag caaaaccaag ctgaagaact tcctacggga ggtgagcatc 300
 33 accaacagcc tctcctccag ccccttcac tcaaggtct ttgacgtggt ctttgagaca 360
 34 gaggactgct acgtctttgc ccaggagtac gcacctgctg gggacctgtt tgacatcatc 420
 35 cctccccagg tggggctccc tgaggacacg gtgaagcgt gtgtgcagca gctgggcctg 480
 36 gcgctggact tcatgcacgg gcggcagctg gtgcaccgag acatcaagcc cgagaacgtg 540
 37 ctgctgttgc accgcgagtg ccgcccgtga aagctggccg acttcggcat gacgcgccgc 600
 38 gtgggctgcc gcgtcaagcg cgtgagcggc accatccctt acacggcgcc tgaggtgtgc 660
 39 caggcgggcc gcgcccagcg gctggcggtg gacacgggag tggacgtgtg ggccttcggc 720
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 43 gagegcgcgc gccccagcaa ggaggtgttc cgcttctc tcaagcagct cagctccgag 960
 44 ctgcgcgcgc ggccttcgca ccgcgcgcgc aagccccccg gggaccgccc gcccgccgcc 1020
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 46 agcggctccc ggcgcgcgc cccgcgcgtc gggtcgggtg ccttgcccgt gccggtgccc 1140
 47 gtgcccagtc ccgtgcccgt gcctgtgccc gagcccggc tagctcccca ggggcccccc 1200
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 52 <211> LENGTH: 424
 53 <212> TYPE: PRT
 54 <213> ORGANISM: Homo sapiens
 56 <400> SEQUENCE: 2
 57 Met Ser Val Gly Cys Pro Glu Pro Glu Pro Pro Arg Ser Leu Thr Cys
 58 1 5 10 15

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59 Cys Gly Pro Gly Thr Ala Pro Gly Pro Gly Ala Gly Val Pro Leu Leu
60          20          25          30
61 Thr Glu Asp Met Gln Ala Leu Thr Leu Arg Thr Leu Ala Ala Ser Asp
62          35          40          45
63 Val Thr Lys His Tyr Glu Leu Val Arg Glu Leu Gly Lys Gly Thr Tyr
64          50          55          60
65 Gly Lys Val Asp Leu Val Val Tyr Lys Gly Thr Gly Thr Lys Met Ala
66 65          70          75          80
67 Leu Lys Phe Val Asn Lys Ser Lys Thr Lys Leu Lys Asn Phe Leu Arg
68          85          90          95
69 Glu Val Ser Ile Thr Asn Ser Leu Ser Ser Ser Pro Phe Ile Ile Lys
70          100         105         110
71 Val Phe Asp Val Val Phe Glu Thr Glu Asp Cys Tyr Val Phe Ala Gln
72          115         120         125
73 Glu Tyr Ala Pro Ala Gly Asp Leu Phe Asp Ile Ile Pro Pro Gln Val
74          130         135         140
75 Gly Leu Pro Glu Asp Thr Val Lys Arg Cys Val Gln Gln Leu Gly Leu
76 145         150         155         160
77 Ala Leu Asp Phe Met His Gly Arg Gln Leu Val His Arg Asp Ile Lys
78          165         170         175
79 Pro Glu Asn Val Leu Leu Phe Asp Arg Glu Cys Arg Arg Val Lys Leu
80          180         185         190
81 Ala Asp Phe Gly Met Thr Arg Arg Val Gly Cys Arg Val Lys Arg Val
82          195         200         205
83 Ser Gly Thr Ile Pro Tyr Thr Ala Pro Glu Val Cys Gln Ala Gly Arg
84          210         215         220
85 Ala Asp Gly Leu Ala Val Asp Thr Gly Val Asp Val Trp Ala Phe Gly
86 225         230         235         240
87 Val Leu Ile Phe Cys Val Leu Thr Gly Asn Phe Pro Trp Glu Ala Ala
88          245         250         255
89 Ser Gly Ala Asp Ala Phe Phe Glu Glu Phe Val Arg Trp Gln Arg Gly
90          260         265         270
91 Arg Leu Pro Gly Leu Pro Ser Gln Trp Arg Arg Phe Thr Glu Pro Ala
92          275         280         285
93 Leu Arg Met Phe Gln Arg Leu Leu Ala Leu Glu Pro Glu Arg Arg Gly
94          290         295         300
95 Pro Ala Lys Glu Val Phe Arg Phe Leu Lys His Glu Leu Thr Ser Glu
96 305         310         315         320
97 Leu Arg Arg Arg Pro Ser His Arg Ala Arg Lys Pro Pro Gly Asp Arg
98          325         330         335
99 Pro Pro Ala Ala Gly Pro Leu Arg Leu Glu Ala Pro Gly Pro Leu Lys
100         340         345         350
101 Arg Thr Val Leu Thr Glu Ser Gly Ser Gly Ser Arg Pro Ala Pro Pro
102         355         360         365
103 Ala Val Gly Ser Val Pro Leu Pro Val Pro Val Pro Val Pro Val Pro
104         370         375         380
105 Val Pro Val Pro Val Pro Glu Pro Gly Leu Ala Pro Gln Gly Pro Pro
106 385         390         395         400
107 Gly Arg Thr Asp Gly Arg Ala Asp Lys Ser Lys Gly Gln Val Val Leu

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110                               420
112 <210> SEQ ID NO: 3
113 <211> LENGTH: 1473
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115 <213> ORGANISM: Homo sapiens
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120 gcgtgggctg cccagagcct gagccgcccc gtcacctgac ctgctgtggg ccggggactg      180
121 cccctgggcc tggtgccggt gtgccccctc tcaactgaaga catgcaggcc ctgactctcc      240
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123 gcacctatgg gaaggttgac ctggtggtct acaagggcac aggcacaaaa atggcactga      360
124 agtttgtgaa caagagcaaa accaagctga agaacttcct acgggaggtg agcatcacca      420
125 acagcctctc ctccagcccc ttcattcatca aggtctttga cgtggtcttt gagacagagg      480
126 actgctacgt ctttgcccag gactacgcac ctgctgggga cctgtttgac atcatccctc      540
127 cccaggtggg gctccctgag gacacggtga agcgtgtgt gcagcagctg ggcctggcgc      600
128 tggacttcat gcacgggcgg cagctggtgc accgcgacat caagcccagg aacgtgctgc      660
129 tgttcgaccg cgagtggcgc cgcgtaaaagc tggccgactt cggcatgacg cgccgcgtgg      720
130 gctgccgcgt caagcgcgtg agcggcacca tcccttacac ggcgcctgag gtgtgccagg      780
131 cgggccgcgc cgacgggctg gcggtggaca cgggcgtgga cgtgtgggoc ttcggcgtgc      840
132 tcatcttctg cgtgctcacc ggcaacttcc cgtgggaggc ggcgtcgggc gccgacgcct      900
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134 gccgcttcac cgagcccgcg ctgcgcattgt tccagcgtt actggccctg gagcccagac      1020
135 gccgcggccc agccaaggag gtgttccgct tcccaagca cgagctcagc tccgagctgc      1080
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138 gtcgccggcc cgcgcccccc gccgtcgggt cgggtgccctt gcccggtgcg gtgccgggtgc      1260
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140 ggaccgacgg ccgcgcggac aagagcaaaag ggcaggtggt gctggccacg gccatcgaga      1380
141 tctgcgtctg agtcgcctcc gccgccctcg gacccgggag cagcccgggc ccgcccagag      1440
142 ccggtgcccc gtgcggcggt agggaaatgga gcc                                1473

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VERIFICATION SUMMARY

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L:15 M:270 C: Current Application Number differs, Replaced Current Application No

L:15 M:271 C: Current Filing Date differs, Replaced Current Filing Date